

Amendments to the Specification

Please amend the Specification to read as follows:

Replace the CROSS-REFERENCE TO RELATED APPLICATIONS section in the Specification of the above-identified application with the following paragraph:

This application is a divisional of Application Number 09/513,775, filed February 25, 2000, now U.S. Patent No. 6,693,228, which claimed priority from provisional patent application Ser. No. 60/121,572 filed February 25, 1999, and provisional patent application Ser. No. 60/123,455 filed March 9, 1999.

Replace the STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT section in the Specification of the above-identified application with the following paragraph:

~~To be determined.~~ This invention was made with United States government support awarded by the following agencies: USDA USDA/CSREES 95-37100-1614. The United States government has certain rights in this invention.

Replace the third paragraph on page 6 (lines 16-25) in the Specification of the above-identified application with the following paragraph:

Set forth below is the nucleotide and amino acid sequences for several FLC genes. The work that gave rise to this document began with the isolation and sequencing of a gene from *Arabidopsis thaliana*, here named FLC1. Using that information and other genetic information, some of which is discussed below, several other FLC genes were discovered. It turns out that *Arabidopsis*, which is extensively studied in plant genetic laboratories since it has one of the smallest genomes of all plants, has at least three FLC genes, here designated FLC1 (SEQ ID NO: 1), FLC2 (SEQ ID NO: 3) and FLC3 (SEQ ID NO:5). Using the information from the three FLC gene found in *Arabidopsis*, two FLC genes from *Brassica* (SEQ ID NO: 7 and 9) have been identified so far. These genes have several characteristics which will be shared by all other plant FLC genes.

Application No.: 10/600,948
Amendment Dated: March 22, 2007
Reply to Office Action Dated: January 4, 2007

Replace the second paragraph on page 7 (lines 10-25) in the Specification of the above-identified application with the following paragraph:

Set forth below in the sequence listing is the cDNA sequence, and the deduced amino acid sequence, for each of FLC1 (SEQ ID NO: 1 and 2), FLC2 (SEQ ID NO: 3 and 4) and FLC3 (SEQ ID NO: 5 and 6) from *Arabidopsis thaliana*, as well as BrFLC1A (SEQ ID NO: 7 and 8) and BrFLC1B (SEQ ID NO: 9 and 10) from *Brassica rapa*. Also presented below is some sequence comparison data. This data indicates that the FLC1 and FLC2 genes from *Arabidopsis* are 60% identical over their entire length, and still over 50% identical over their entire region outside of the MADS box region. The latter comparison may be more important since all of the MADS box genes have a relatively high degree of conservation in the MADS box region itself. For the purposes of this analysis, the MADS box region is considered to be the first 60 amino acids at the amino terminus of the protein sequences. This degree of sequence similarity appears to hold across species. The Brassica genes BrFLC1a and BrFLC1B are actually more identical to FLC1 than FLC1 is to FLC2. The identity of FLC2 to the Brassica genes is slightly less than 50% outside of the MADS box, so among the variants in the FLC gene family, identity at the amino acid levels is likely to generally be above 40%. Thus, amino acid identity of over 40% outside the MADS box regions is one indication of a member of the FLC gene family.